⧣ 2   OIPE

RAW SEQUENCE LISTING   DATE: 07/19/2001
PATENT APPLICATION: US/09/895,435   TIME: 15:50:45

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Output Set: N:\CRF3\07192001\I895435.raw   ENTERED

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  3 <110> APPLICANT: Stewart, A. F.
  4        Zhang, Y.
  5        Hallet, B.
  7 <120> TITLE OF INVENTION: A New Tyrosine Recombinase for Genetic Engineering
  9 <130> FILE REFERENCE: 9882-012-999
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/895,435
C--> 11 <141> CURRENT FILING DATE: 2001-06-30
 11 <160> NUMBER OF SEQ ID NOS: 10
 13 <170> SOFTWARE: PatentIn version 3.0
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 16 <211> LENGTH: 244
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Bacillus thuringiensis
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 23 caatattaat tgtgttgtat taggtgttat aataaatata aatctagggg tttaacgcaa       180
 24 cacaatttat cgataaataa atactttag acgcaacaca atttatagac gcggaggaaa        240
 25 tcac                                                                    244
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 30 <213> ORGANISM: Bacillus thuringiensis
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 36 <210> SEQ ID NO: 3
 37 <211> LENGTH: 32
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Bacillus thuringiensis
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 45 <211> LENGTH: 249
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Bacillus thuringiensis
 49 <400> SEQUENCE: 4
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 51 aaaatatatc attattcctt gacacataca tgttcttttt ttatacaaaa aataatacaa       120
 52 cacaatatta attgtgttgt attaggtgtt ataataaata taaatctagg ggtttaacgc       180
 53 aacacaattt atcgataaat aaatactttt agacgcaaca caatttatag acgcggagga       240
 54 aatcacatg                                                               249
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63 <222> LOCATION: (1)..(798)
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68 1               5                   10                  15
69 acc gag aac act gtt cag gga tac aca tca ggt att aga cag tac ata        96
70 Thr Glu Asn Thr Val Gln Gly Tyr Thr Ser Gly Ile Arg Gln Tyr Ile
71             20                  25                  30
72 aaa tgg ttt gaa ggt tcc tat gac aga aaa ttg aca aaa ttg tac cga       144
73 Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg
74         35                  40                  45
75 caa aat atc tta gag tac att agt tat tta aag aat gtc aaa atg ttg       192
76 Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu
77     50                  55                  60
78 aac gcc aag tcc att aac cac aag att agt agc ctt gct aaa ttt aat       240
79 Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn
80 65                  70                  75                  80
81 gaa ttt cta ata cag aaa gga agt caa caa gat caa gta att tta tta       288
82 Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu
83                 85                  90                  95
84 gat gta aaa aag ttt tta caa agt gtg tta gag gat aat aac aaa cgt       336
85 Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg
86             100                 105                 110
87 aat tat gca att gcc act ctc cta gca tat aca gga gta cgt att tca       384
88 Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser
89         115                 120                 125
90 gag gca tta tct atc aaa atg aat gac ttc aat tta cag act ggg gaa       432
91 Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu
92     130                 135                 140
93 tgt att att cga agt gga aaa gga ggt aaa caa cga att gta tta cta       480
94 Cys Ile Ile Arg Ser Gly Lys Gly Gly Lys Gln Arg Ile Val Leu Leu
95 145                 150                 155                 160
96 aat agt aag gta ctt agt gct atc aaa gat tat ctc atc gat cga aaa       528
97 Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys
98                 165                 170                 175
99 aca tac agt aca gca cat gaa tct ccg tat ctt ttt att agt aaa aag       576
100 Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys
101             180                 185                 190
102 cga gaa aag ctc gac cgt acg gtc gtc aat cgt atc ttt aaa tca tac       624
103 Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr
104             195                 200                 205
105 agg aat gtt att act cca cac caa tta cga cac ttc ttc tgt acg aat       672
106 Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn
107     210                 215                 220
108 gca att caa aaa gga ttt agc att cat gaa gtt gca aat caa gct ggg       720
109 Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly
110 225                 230                 235                 240
111 cac tct aac atc cat acg aca cta ctt tac aca aat cca aac caa ctg       768
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112 His Ser Asn Ile His Thr Thr Leu Leu Tyr Thr Asn Pro Asn Gln Leu
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119 <211> LENGTH: 265
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128             20              25              30
130 Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg
131         35              40              45
133 Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu
134     50              55              60
136 Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn
137 65              70              75              80
139 Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu
140             85              90              95
142 Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg
143             100             105             110
145 Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser
146         115             120             125
148 Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu
149     130             135             140
151 Cys Ile Ile Arg Ser Gly Lys Gly Gly Lys Gln Arg Ile Val Leu Leu
152 145             150             155             160
154 Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys
155             165             170             175
157 Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys
158             180             185             190
160 Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr
161         195             200             205
163 Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn
164     210             215             220
166 Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly
167 225             230             235             240
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176 <211> LENGTH: 116
177 <212> TYPE: DNA
178 <213> ORGANISM: Bacillus thuringiensis
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181 taatacaaca caatattaat tgtgttgtat taggtgttat aataaatata tatctagggg      60
182 tttaacgcaa cacaatttat cgataaataa atacttttag acgcaacaca atttat          116
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185 <211> LENGTH: 116
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187 <213> ORGANISM: Bacillus thuringiensis
189 <400> SEQUENCE: 8
190 taatacaaca caatattaat tgtgttgtat taggtgttat aatatatata aatctagggg      60
191 tttaacgcaa cacaatttat cgataaataa atacttttag acgcaacaca atttat          116
193 <210> SEQ ID NO: 9
194 <211> LENGTH: 116
195 <212> TYPE: DNA
196 <213> ORGANISM: Bacillus thuringiensis
198 <220> FEATURE:
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200 <222> LOCATION: 33 .. 64
201 <223> OTHER INFORMATION: n = a, t, g, or c
203 <221> NAME/KEY: N_region
204 <222> LOCATION: 81 .. 100
205 <223> OTHER INFORMATION: n = a, t, g, or c
207 <400> SEQUENCE: 9
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209 nnnnacgcaa cacaatttat nnnnnnnnnn nnnnnnnnnn acgcaacaca atttat          116
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212 <211> LENGTH: 124
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214 <213> ORGANISM: Bacillus thuringiensis
217 <220> FEATURE:
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219 <222> LOCATION: 33 .. 74
220 <223> OTHER INFORMATION: n = a, t, g, or c
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225 ttta                                                                  124
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VERIFICATION SUMMARY   DATE: 07/19/2001
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10